Using a Massive Agent-based Model to Study the Spread of Pandemic Influenza

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An influenza pandemic has great potential to cause large and rapid global and domestic increases in deaths and serious illness. Mathematical models and computer simulations have become the standard approach to studying epidemics. Recent analyses of nationwide pandemic dynamics [1,2] used detailed social contact models along with geospatial population density and travel patterns to develop agent-based models. However, they took average household size to be geospatially uniform, causing them to under-predict the variation and clustering of pandemic severity. Furthermore, they ignored the potential impact of temporary community-based strategies such as school closures.

We used the highly structured Epidemic Simulation System (EpiSimS) to simulate the detailed person-to-person contact of 19 million synthetic individuals representing the residents of Southern California. The EpiSimS agent-based discrete event engine [3] can simulate influenza pandemics at sufficient fidelity to capture geospatially varying demographic characteristics, travel patterns of individuals, and transmission opportunities through household, work, school, social, and casual contacts. We simulated a moderately severe influenza pandemic on a geographic stratum of 2.3 million locations, representing a six-county region of Southern California (Los Angeles, Orange, Riverside, San Bernardino, Ventura, and San Diego counties). Parameters describing the progression and transmission of influenza are based on [4]. Simulations were run on the Coyote cluster, an Institutional Computing resource.

The aggregate attack rate over the 3978 census tracts in the six counties is 30.6%, with a standard deviation of 7.5%. Figure 1 shows the attack rate for each census tract. The R-squared value of the *Pearson product moment correlation coefficient* between average household size and attack rate by tract is 0.90. Thus 90% of the variation in the attack rate by census tract is attributable to the average household size characteristic of the tract.

Results also demonstrate that temporary behavioral changes have the potential to generate waves, if they are relaxed before the pandemic dies out. The model
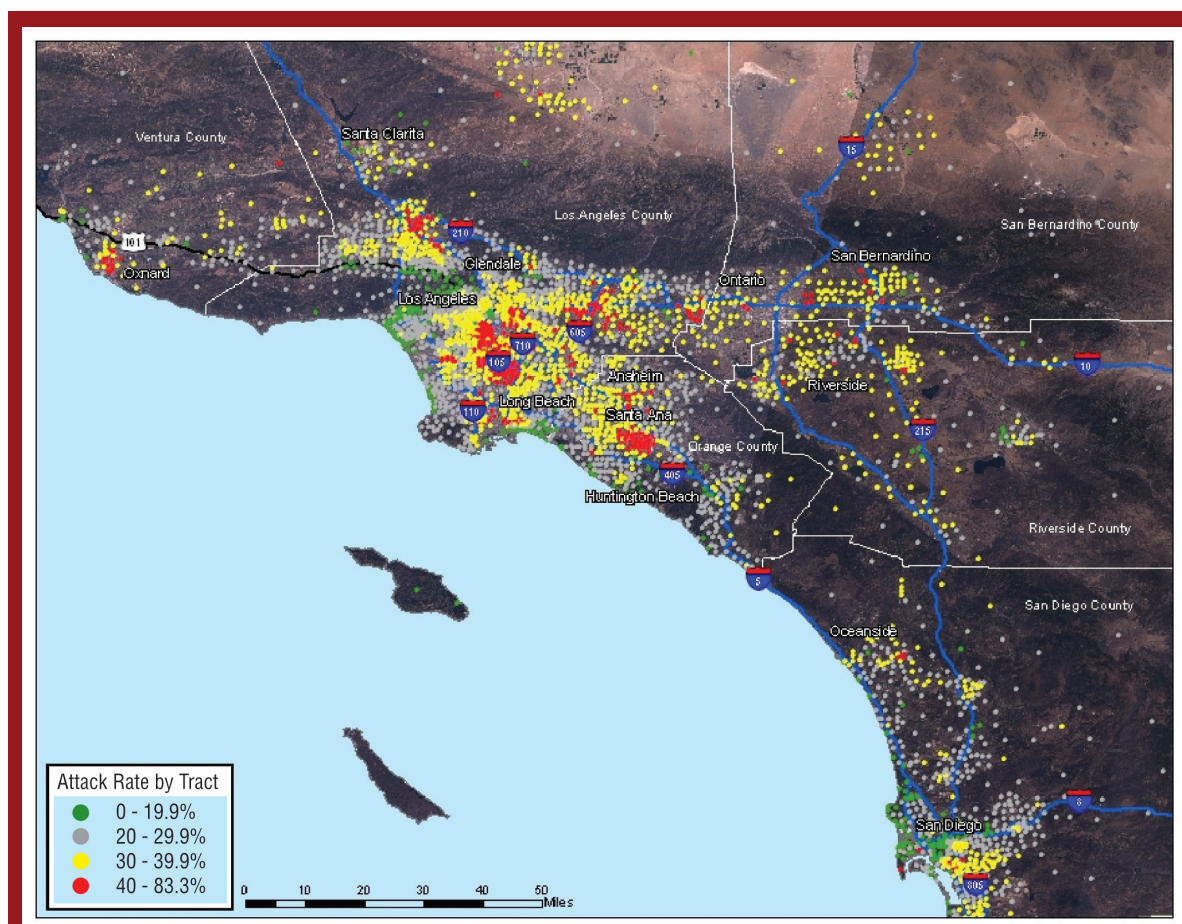

Fig. 1. The results of an individual-based stochastic model of the pandemic influenza in Southern California. The hot-spots are strongly correlated with regions of high average household size.

predicts that if school closures are implemented for the duration of the pandemic, the clinical attack rate could be reduced by more than 50%. Figure 2 shows the symptomatic percentage of the population as a function of time for the baseline and 100% school closures for 5, 8, and 11 months.

Our results are useful in providing guidance on the effects of school closures and deployment of limited resources. Readily available household-size statistics can be used to identify communities that are prone to higher-than-average attack rates. National or regional spatiotemporal pandemic simulation used to support influenza response planning should retain the geographic variation of demographic factors.

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[1] T.C. German, et al., *PNAS,* **103**(15), 5935-5940 (2006).
[2] N.M. Ferguson, et al., *Nature,* **442,** 448-452 (2006).
[3] P.D. Stroud, et al., *J Artif Soc Soc Simulat,* **10**(4) 9 (2007).
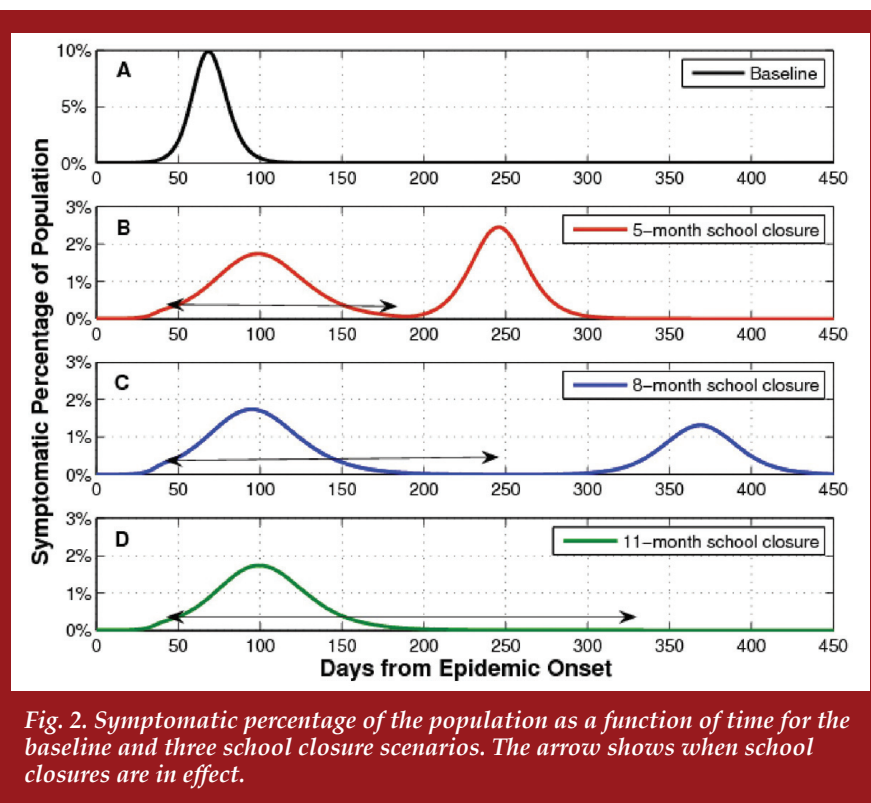[4] I.M. Longini, et al., *Am J Epidemiol,* **159**(7), 623-33 (2004).

Fig. 2. Symptomatic percentage of the population as a function of time for the baseline and three school closure scenarios. The arrow shows when school closures are in effect.